



SEQUENCE LISTING

<110> Kaplan, Aaron
Lieman-Hurwitz, Judy
Schatz, Daniella
Mittler, Ron
Ronen-Tarazi, Michal
Bonfil, David J.

<120> ENHANCING INORGANIC CARBON FIXATION BY PHOTOSYNTHETIC ORGANISMS

<130> 01/22171

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 4957

<212> DNA

<213> Synechococcus sp.

<400> 1
aagcttggat tgaagcgatc ggggtcaatc ccagcgatga tcctcagttc ctectgatgg 60
tcgatccctt tagcgccaag attgaggatc tgctgcaagg gctggatttc gcctatcccg 120
aggccgtgaa agtgggcgga ttggccagtg gtttgggggc agagtcagcg atcgccagct 180
tgttttttca agaccgacag gtcgatggcg tgattgggct agccctcagt ggcaatgtcc 240
agctgcaggc gatcgtggct cagggtgtgc gtccagttgg cccgctttgg catgtggcag 300
cggcggagcg caacattctg cggcaacttc agaccgaaga cgaggaaccg atcgccgcgc 360
tgcaagccct acagtcagtc ctgcgtgac tctcccctga attacagcga tcgctctgtg 420
tgggcctggc ctgcaattct ttccaaacgg tattacaacc gggcgacttc ctgatccgta 480
acctgctggg gtttgatccc cgcactgggtg ctgtagcaat cggcgatcgc attcgagttg 540
ggcagcggct gcagctgcac gtacgggatg cccagacagc ggcggatgac ctcgagcggc 600

aactgggggea atgggtgccgg cagcatgcga caaaaccagc agcttccctc ttgttttccct	660
gcttgggggcg cggcaagccc ttctatcagc aggccaactt cgagtcgcaa ctgattcagc	720
attacctctc agagctgccc ctagctggct ttttctgtaa tggcgaaatc ggcccgatcg	780
ctggcagcac ctacctgcat ggctacacat cggtgctggc tttgctgtcg gccaaaactc	840
actagcgcca gcgagacctg attgtcgatc tgctgagcgc gactgtagcg ctggaaatag	900
gcccggacct gagcaggcgc atcgccaag ctgaccgtag tatcacctc agccaccccc	960
gcccagaaat tccgcaacat cggcaggaga gcgatcgct ccgcctccga taaattcaac	1020
ggctcatggg tcaacaggcg gatcaagtac tctgactgcg atcgccatcc attcccgcgcg	1080
aaaacgtttg taaatcagtc ttgatccggt agcgatcgca cccgacggga ctctagttct	1140
agttgccaac cttcagcggc aggttgtagc gttccgagtc ggtagggatg gggatagctg	1200
accaaggaac cggtcgtgac ttcccagaga gcaccttgct gactgggtggc ttggatgtgg	1260
aggtggcctg tgaagatcac cgagacgctg ccgccttcga ggattgatcg caattcctcg	1320
gcattttcta agatgtagcg ctgaccaagc ggatgctgct gttgatcggg cagatgctcc	1380
aacacattgt ggtgaatcat caccacgctg tggctagcgg tggaagtggc gagttcttgt	1440
tgcagccagt tgagttgcgc gcaatcgact cgcctccgat gcagttgatg gcccgcttca	1500
tcaaaagcga tcgaattcag cgcaaacaga tcgagatccg gtgcgatcgt gcagcgatag	1560
taggggcgat cgctcgtgaa gccaaagtct tgatagagct cgacaaactc ggccacaccg	1620
gtgcgatcgc gatcgctcgc tgcggcgggc atatcgtggt tgcccggcac cacatagacc	1680
ggatagggca actggcgcaa ttgttgtagc agccactgat ggttttcccg ctccccgtgc	1740
tgggttaaatt cccccggcag caacaggaag tccaaatcca gcgctgccag ttctgtcagg	1800
atttgctcaa aagccggaat gctgcactca atcaaatgga agcgatgggg atggtgcaa	1860
attgtctgcg gcagtccaat gtggagatcg ctcagcagcg caaatcgaaa cgctcgggtc	1920
attgccatcc cctcagctat cgagcccgat tctaggcgaa gctaggtcga gtccgttgtc	1980
ttcagttgca agcattcatg gccagagttc gcgttcggca gcacgtcaat ccgctctctc	2040
agaaattcca agtggtcacg acttggccgg attggcaaca ggtctatgcg gactgcgac	2100
gcccgtgca tttggatatt ggctgtgctc gcgggcgctt tctgctggca atggcgacac	2160
gacaacctga gtggaattat ctggggctgg aaattcgtga gccgctggta gatgaggcga	2220
acgcgatcgc ccgcgaacgt gaactgacca atctctacta ccacttcagc aacgccaatt	2280
tggacttgga accgctgctg cgatcgctgc cgacagggat tttgcagcgg gtcagcattc	2340
agttcccgga tccttggttc aagaaacgcc atcaaaagcg acgcgtcgtc cagccggaac	2400
tggtgcaagc cctcgcgact gcgttacctg ctggtgcaga ggtctttctg caatccgatg	2460
tgctggaagt gcaggcagag atgtgcgaac actttgcggc ggaacccgcg tttcagcgca	2520

cctgcttgga	ctggctgccg	gaaaatccgc	tgcccgtccc	gaccgagcgc	gaaattgccg	2580
ttcaaaacaa	acagttgcca	gtctaccgtg	ctctcttcat	tccgcagcca	gcggactaag	2640
ctcttaaggc	aagcgttgac	gcgatcgcca	tgactgtctg	gcaaactctg	acttttgccc	2700
attaccaacc	ccaacagtgg	ggccacagca	gtttcttgca	tccgctgttt	ggcagcctgc	2760
gagcttgccg	ggcctccagc	cagctgttgg	tttggctctga	ggcactgggt	ggcttcttgc	2820
ttgctgtcgt	ctacggttcg	gctccgtttg	tgcccagttc	cgccctaggg	ttggggctag	2880
ccgcgatcgc	ggcctattgg	gccctgctct	cgtgacaga	tatcgatctg	cggcaagcaa	2940
ccccattca	ctggctgggtg	ctgctctact	ggggcgtcga	tgccctagca	acgggactct	3000
cacccgtagc	cgtgcagct	ttagttgggc	tagccaaact	gacgctctac	ctgttggttt	3060
ttgccctagc	ggctcgggtt	ctccgcaatc	cccgtctgcg	atcgctgctg	ttctcggtcg	3120
tctgatcac	atcgcttttt	gtcagtgtct	acggcctcaa	ccaatggatc	tacggcgttg	3180
aagagctggc	gacttgggtg	gatcgcaact	cggttgccga	cttcacctca	cgggtttaca	3240
gctatctggg	caaccccaac	ctgctggctg	cttatctggt	gccgacgact	gccttttctg	3300
cagcagcgat	cgggggtgtg	cgcggctggc	tccccaagct	gctggcgatc	gctgcgacag	3360
gtgcgagcag	cttatgtctg	atcctcacct	acagtcgcgg	tggctggctg	ggttttgtcg	3420
ccatgatatt	tgtctggggc	ttattagggc	tctactgggt	tcaaccccgt	ctacccgcac	3480
cctggcgacg	ctggctattc	ccagtcgtat	tgggtggact	agtcgcgggtg	ctcttgggtg	3540
cgggtgcttg	acttgagccg	ttgcgcgtgc	gcgtgttgag	catctttgtg	gggcgtgaag	3600
acagcagcaa	caacttcggg	atcaatgtct	ggctggcggg	gctgcagatg	attcaagatc	3660
ggccttggct	gggcatcggc	cccggcaata	ccgcctttaa	cctggtttat	cccctctatc	3720
aacaggcgcg	ctttaaggcg	ttgagcgctt	actccgtccc	gctggaagtc	gcggttgagg	3780
gcggactact	gggcttgacg	gccttcgctt	ggctgctgct	ggtcacggcg	gtgacggcgg	3840
tgcggcaggt	gagccgactg	cggcgcgatc	gcaatcccca	agccttttgg	ttgatggcta	3900
gcttggccgg	tttggcagga	atgctgggtc	acggtctgtt	tgataccgtg	ctctatcgac	3960
cggaagccag	tacgctctgg	tggctctgta	ttggagcgat	cgcgagtttc	tggcagcccc	4020
aaccttccaa	gcaactccct	ccagaagccg	agcattcaga	cgaaaaaatg	tagcgggctc	4080
cccaacaaat	tcctgtgcac	ccgactggat	ccaccaccta	aactggatcc	caaaggtatc	4140
cgggtgatct	agggtcataa	cgaactccga	ccgcgatcgc	gtccgcgaac	tgaacctcca	4200
tcgcaccgaa	gcggagtctg	ttagtcgttg	aagagccaat	gctagagggg	gctgccgaag	4260
cagttgggct	ggaagcaggc	tgcgagaagc	caccgcgcatc	caaggcaaag	ttcagccgac	4320
cttccgcaaa	gactacgatc	gccacggcgg	ctctgccagc	taagtcagcg	ctgggttagt	4380
tgtcatagca	gtccgcagac	aagttaggac	aacttcatag	agggactcgc	tcagagtcaa	4440

cagccgctgt ccgtgggggt gcgcaatcac cccacacccc acgcactggg ggactcgact 4500
 ccccagggcc ccccgcaaca agatttcgga taaggggcat cggctgaatc gcgatcgctg 4560
 cgggtaaaac tagccggtgt tagccatggg tttgagacta atcggcacgg ggcaaaacgt 4620
 cctgatttat ttgctcaatg tgataggtta catcgtcaaa aacaaggccc aagaggtagg 4680
 aaaaatcacg accgccaag tccgagggtt ttgctgttgg gagcgaccta gggcagacta 4740
 gacagagcat tgctgtgagc caaagcgctt tcaattgctg gcggctgtgg gtttttcgga 4800
 gggtgcaaaa tgaaagacct ttctgtcaat gtctctcgct atccccgcta cttcatcacc 4860
 ttccagctgg gtatttttta gtcgatctac cagtgggtgc ggccgatggg tcgcaaccca 4920
 gtcgcggctt gggcgctgct aggccttgga gtttcga 4957

<210> 2

<211> 1404

<212> DNA

<213> *Synechococcus* sp.

<400> 2

atgactgtct ggcaaactct gacttttgcc cattaccaac cccaacagtg gggccacagc 60
 agtttcttgc atcggtgtt tggcagcctg cgagcttggc gggcctccag ccagctgttg 120
 gtttggtctg aggcactggg tggtttcttg cttgctgtcg tctacggttc ggctccgttt 180
 gtgcccagtt ccgccctagg gttggggcta gccgcgatcg cggcctattg ggcctgctc 240
 tcgctgacag atatcgatct gcggcaagca accccattc actggctggg gctgctctac 300
 tggggcgctc atgccctagc aacgggactc tcaccgctac gcgctgcagc tttagttggg 360
 ctagccaaac tgacgctcta cctgttggtt tttgccctag cggctcgggt tctccgcaat 420
 ccccgctcgc gatcgctgct gttctcggtc gtcgtgatca catcgctttt tgtcagtgtc 480
 tacggcctca accaatggat ctacggcgtt gaagagctgg cgacttgggt ggatcgcaac 540
 tcggttgccg acttcacctc acgggtttac agctatctgg gcaaccccaa cctgctggct 600
 gcttatctgg tgccgacgac tgccctttct gcagcagcga tcgggggtgtg gcgcggctgg 660
 ctccccaagc tgctggcgat cgctgcgaca ggtgcgagca gcttatgtct gatcctcacc 720
 tacagtcgcg gtggctggct gggttttgtc gccatgattt ttgtctgggc gttattaggg 780
 ctctactggg ttcaaccccg tctaccgca ccctggcgac gctggctatt ccagtcgta 840
 ttgggtggac tagtcgcggt gctcttggtg gcggtgcttg gacttgagcc gttgcgcgtg 900
 cgcgtgttga gcatctttgt ggggcgtgaa gacagcagca acaacttccg gatcaatgtc 960
 tggctggcgg tgctgcagat gattcaagat cggccttggc tgggcatcgg ccccggaat 1020

```

accgccttta acctggttta tcccctctat caacaggcgc gctttacggc gttgagcgcc 1080
tactccgtcc cgctggaagt cgcggttgag ggcggactac tgggcttgac ggccttcgct 1140
tggctgctgc tggtcacggc ggtgacggcg gtgcggcagg tgagccgact gcggcgcgat 1200
cgcaatcccc aagccttttg gttgatggct agcttggccg gtttggcagg aatgctgggt 1260
cacggtctgt ttgataccgt gctctatcga ccggaagcca gtacgctctg gtggctctgt 1320
attggagcga tcgcgagttt ctggcagccc caaccttcca agcaactccc tccagaagcc 1380
gagcattcag acgaaaaaat gtag 1404

```

<210> 3

<211> 467

<212> PRT

<213> *Synechococcus* sp.

<400> 3

```

Met Thr Val Trp Gln Thr Leu Thr Phe Ala His Tyr Gln Pro Gln Gln
1          5          10         15

Trp Gly His Ser Ser Phe Leu His Arg Leu Phe Gly Ser Leu Arg Ala
20          25          30

Trp Arg Ala Ser Ser Gln Leu Leu Val Trp Ser Glu Ala Leu Gly Gly
35          40          45

Phe Leu Leu Ala Val Val Tyr Gly Ser Ala Pro Phe Val Pro Ser Ser
50          55          60

Ala Leu Gly Leu Gly Leu Ala Ala Ile Ala Ala Tyr Trp Ala Leu Leu
65          70          75          80

Ser Leu Thr Asp Ile Asp Leu Arg Gln Ala Thr Pro Ile His Trp Leu
85          90          95

Val Leu Leu Tyr Trp Gly Val Asp Ala Leu Ala Thr Gly Leu Ser Pro
100         105         110

Val Arg Ala Ala Ala Leu Val Gly Leu Ala Lys Leu Thr Leu Tyr Leu
115         120         125

Leu Val Phe Ala Leu Ala Ala Arg Val Leu Arg Asn Pro Arg Leu Arg
130         135         140

```

Ser Leu Leu Phe Ser Val Val Val Ile Thr Ser Leu Phe Val Ser Val
 145 150 155 160

Tyr Gly Leu Asn Gln Trp Ile Tyr Gly Val Glu Glu Leu Ala Thr Trp
 165 170 175

Val Asp Arg Asn Ser Val Ala Asp Phe Thr Ser Arg Val Tyr Ser Tyr
 180 185 190

Leu Gly Asn Pro Asn Leu Leu Ala Ala Tyr Leu Val Pro Thr Thr Ala
 195 200 205

Phe Ser Ala Ala Ala Ile Gly Val Trp Arg Gly Trp Leu Pro Lys Leu
 210 215 220

Leu Ala Ile Ala Ala Thr Gly Ala Ser Ser Leu Cys Leu Ile Leu Thr
 225 230 235 240

Tyr Ser Arg Gly Gly Trp Leu Gly Phe Val Ala Met Ile Phe Val Trp
 245 250 255

Ala Leu Leu Gly Leu Tyr Trp Phe Gln Pro Arg Leu Pro Ala Pro Trp
 260 265 270

Arg Arg Trp Leu Phe Pro Val Val Leu Gly Gly Leu Val Ala Val Leu
 275 280 285

Leu Val Ala Val Leu Gly Leu Glu Pro Leu Arg Val Arg Val Leu Ser
 290 295 300

Ile Phe Val Gly Arg Glu Asp Ser Ser Asn Asn Phe Arg Ile Asn Val
 305 310 315 320

Trp Leu Ala Val Leu Gln Met Ile Gln Asp Arg Pro Trp Leu Gly Ile
 325 330 335

Gly Pro Gly Asn Thr Ala Phe Asn Leu Val Tyr Pro Leu Tyr Gln Gln
 340 345 350

Ala Arg Phe Thr Ala Leu Ser Ala Tyr Ser Val Pro Leu Glu Val Ala
 355 360 365

Val Glu Gly Gly Leu Leu Gly Leu Thr Ala Phe Ala Trp Leu Leu Leu
 370 375 380

Val Thr Ala Val Thr Ala Val Arg Gln Val Ser Arg Leu Arg Arg Asp
 385 390 395 400

Arg Asn Pro Gln Ala Phe Trp Leu Met Ala Ser Leu Ala Gly Leu Ala
 405 410 415

Gly Met Leu Gly His Gly Leu Phe Asp Thr Val Leu Tyr Arg Pro Glu
 420 425 430

Ala Ser Thr Leu Trp Trp Leu Cys Ile Gly Ala Ile Ala Ser Phe Trp
 435 440 445

Gln Pro Gln Pro Ser Lys Gln Leu Pro Pro Glu Ala Glu His Ser Asp
 450 455 460

Glu Lys Met
 465

<210> 4

<211> 1425

<212> DNA

<213> Synechococcus sp.

<400> 4

atggtgtctc ccatctctat ctggcgatcg ctgatgtttg gcggtttttc cccccaggaa	60
tggggccggg gcagtgtgct ccatcgtttg gtgggctggg gacagagttg gatacaggct	120
agtgtgctct ggccccactt cgaggcattg ggtacggctc tagtggcaat aatttttatt	180
gcggctccct tcacctccac caccatgttg ggcattttta tgctgctctg tggagccttt	240
tgggctctgc tgacctttgc tgatcaacca gggaagggtt tgactcccat ccatgtttta	300
gtttttgcct actggtgcat ttcggcgatc gccgtgggat tttctccggt aaaaatggcg	360
gcggcgtcgg ggtagcgaa attaacagct aatttatgtc tgtttctact ggcggcgagg	420
ttattgcaaa acaaacaatg gttgaaccgg ttagtaaccg ttgttttact ggtagggcta	480
ttggtgggga gttacggtct gcgacaacag gtggacgggg tagaacagtt agccacttgg	540
aatgacccca cctctacctt ggcccaggcc actaggggtat atagcttttt aggtaatccc	600
aatctcttgg cggettacct ggtgcccattg acgggtttga gcttgagtgc cctggtggta	660
tggcgacggt ggtggcccaa actgctggga gcaaccatgg tgattgttaa cctactctgt	720
ctctttttta cccagagccg gggcggttgg ctagcagtgc tggccctggg agctaccttc	780
ctggcccttt gttacttctg gtggttacct caattacca aattttggca acggtggtct	840
ttgcccctgg cgatcgccgt ggcggttata ttaggtgggg gagcgttgat tgcggtggaa	900
ccgattcgac tcagggccat gagcattttt gctgggcggg aagacagcag taataatttc	960
cgcataatg tttgggaagg ggtaaaagcc atgatccgag cccgccctat cattggcatt	1020

```

ggcccaggta acgaagcctt taaccaaatt tatecttact atatgcggcc ccgcttcacc 1080
gccctgagtg cctattccat ttacctagaa attttggtgg aaacgggtgt agttgggttt 1140
acctgtatgc tctggctgtt ggccgttacc ctaggcaaag gcgtagaact ggtaaacgc 1200
tgtcgcaaaa ccctcgcccc ggaaggcatc tggattatgg gggctttagc ggcgatcatc 1260
ggtttggttg tccacggcat ggtagatata gtctggtacc gtcccccggt gagcactttg 1320
tggtggttgc tagtggccat tggtgctagt cagtgggcca gcgccaggc ccgtttggag 1380
gccagtaaag aagaaaatga ggacaaacct cttcttgctt cataa 1425

```

<210> 5

<211> 474

<212> PRT

<213> Synechococcus sp.

<400> 5

```

Met Val Ser Pro Ile Ser Ile Trp Arg Ser Leu Met Phe Gly Gly Phe
1           5           10          15
Ser Pro Gln Glu Trp Gly Arg Gly Ser Val Leu His Arg Leu Val Gly
20          25          30
Trp Gly Gln Ser Trp Ile Gln Ala Ser Val Leu Trp Pro His Phe Glu
35          40          45
Ala Leu Gly Thr Ala Leu Val Ala Ile Ile Phe Ile Ala Ala Pro Phe
50          55          60
Thr Ser Thr Thr Met Leu Gly Ile Phe Met Leu Leu Cys Gly Ala Phe
65          70          75          80
Trp Ala Leu Leu Thr Phe Ala Asp Gln Pro Gly Lys Gly Leu Thr Pro
85          90          95
Ile His Val Leu Val Phe Ala Tyr Trp Cys Ile Ser Ala Ile Ala Val
100         105         110
Gly Phe Ser Pro Val Lys Met Ala Ala Ala Ser Gly Leu Ala Lys Leu
115         120         125
Thr Ala Asn Leu Cys Leu Phe Leu Leu Ala Ala Arg Leu Leu Gln Asn
130         135         140

```


Lys Gln Trp Leu Asn Arg Leu Val Thr Val Val Leu Leu Val Gly Leu
 145 150 155 160

Leu Val Gly Ser Tyr Gly Leu Arg Gln Gln Val Asp Gly Val Glu Gln
 165 170 175

Leu Ala Thr Trp Asn Asp Pro Thr Ser Thr Leu Ala Gln Ala Thr Arg
 180 185 190

Val Tyr Ser Phe Leu Gly Asn Pro Asn Leu Leu Ala Ala Tyr Leu Val
 195 200 205

Pro Met Thr Gly Leu Ser Leu Ser Ala Leu Val Val Trp Arg Arg Trp
 210 215 220

Trp Pro Lys Leu Leu Gly Ala Thr Met Val Ile Val Asn Leu Leu Cys
 225 230 235 240

Leu Phe Phe Thr Gln Ser Arg Gly Gly Trp Leu Ala Val Leu Ala Leu
 245 250 255

Gly Ala Thr Phe Leu Ala Leu Cys Tyr Phe Trp Trp Leu Pro Gln Leu
 260 265 270

Pro Lys Phe Trp Gln Arg Trp Ser Leu Pro Leu Ala Ile Ala Val Ala
 275 280 285

Val Ile Leu Gly Gly Gly Ala Leu Ile Ala Val Glu Pro Ile Arg Leu
 290 295 300

Arg Ala Met Ser Ile Phe Ala Gly Arg Glu Asp Ser Ser Asn Asn Phe
 305 310 315 320

Arg Ile Asn Val Trp Glu Gly Val Lys Ala Met Ile Arg Ala Arg Pro
 325 330 335

Ile Ile Gly Ile Gly Pro Gly Asn Glu Ala Phe Asn Gln Ile Tyr Pro
 340 345 350

Tyr Tyr Met Arg Pro Arg Phe Thr Ala Leu Ser Ala Tyr Ser Ile Tyr
 355 360 365

Leu Glu Ile Leu Val Glu Thr Gly Val Val Gly Phe Thr Cys Met Leu
 370 375 380

Trp Leu Leu Ala Val Thr Leu Gly Lys Gly Val Glu Leu Val Lys Arg
 385 390 395 400

Cys Arg Gln Thr Leu Ala Pro Glu Gly Ile Trp Ile Met Gly Ala Leu
 405 410 415

Ala Ala Ile Ile Gly Leu Leu Val His Gly Met Val Asp Thr Val Trp
 420 425 430

Tyr Arg Pro Pro Val Ser Thr Leu Trp Trp Leu Leu Val Ala Ile Val
 435 440 445

Ala Ser Gln Trp Ala Ser Ala Gln Ala Arg Leu Glu Ala Ser Lys Glu
 450 455 460

Glu Asn Glu Asp Lys Pro Leu Leu Ala Ser
 465 470

<210> 6

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 6

gggctagccg cgatcgcggc ctattggggc c

31

<210> 7

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 7

gggctaggga tcgcgcttat tgggccc

27

<210> 8

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 8

gggctcagat cgcgcctatt gggccc

26

<210> 9

<211> 11

<212> PRT

<213> Synechococcus sp.

<400> 9

Gly Leu Ala Ala Ile Ala Ala Tyr Trp Ala Leu
1 5 10